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ELUCIDATING THE ROLE OF SMALL NUCLEOLAR RNA 114-12 IN ACUTE PROMYELOCYTIC LEUKEMIA

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Recent studies show a significant dysregulation with functional implications of small non-coding RNAs in patients with acute leukemia (AML). The canonical role of small nucleolar RNAs (snoRNAs), a subcategory of non-coding RNAs, is to modify ribosomal RNA. However, there are orphan snoRNAs without any known ribosomal RNA target. Studies have shown that there is an overexpression of snoRNA114-12 in M3-AML. This study aimed to determine the biological effect of inducing overexpression of snoRNA114-12 in various models. An overexpression system was generated to model the endogenous genic environment from which snoRNAs are normally processed. The construct was then utilized to analyze the effect of snoRNA114-12 overexpression on cellular growth dynamics. Our system successfully and robustly leads to the overexpression and correct processing of various snoRNAs. Our results show that snoRNA114-12 overexpression in K562 cells, an erythroid cell line, induces apoptosis via the intrinsic pathway. Relatedly, ongoing studies are aimed at studying the effect of snoRNA114-12 overexpression in hematopoiesis and proliferation. Preliminary data suggest that snoRNA114-12 confers a granulocytic bias during the differentiation of CD34+ hematopoietic progenitor cells, and is associated with an increase in colony number. Our study provides valuable insights into the effect of snoRNA114-12 overexpression on cellular biology. Overall, our data suggests that snoRNA114-12 induces apoptosis in erythroid precursors and may confer a bias against erythroid differentiation. Further studies will aim to elucidate the mechanisms underlying the contribution of snoRNA114-12 to M3-AML.